Supplemental Table 1

Liposome		Peptide Sequence	Occurrence	Probability in Ph.d.12
PC	PC1	**H W Y D S F V P W G H Q**	16	2.43E-16
	PC2	**I P S P L E F L S E L M**	7	1.20E-15
	PC3	**K M P I P S P A M P F G**	1	3.92E-16
	PC4	**S S A W W S Y W P P V A**	1	4.12E-17
	PC5	**L P L M K T N E Y P D L**	1	1.28E-16
	PC6	**G Y F S P R I S P S P S**	1	1.21E-14
ELM	ELM1	**M H G K V H H P L S P R**	5	1.06E-15
	ELM2	**M G H S H N T P A P K S**	2	2.04E-13
	ELM3	**G H F N K H M R A S V P**	2	8.11E-15
		L T H H T S P P P V P A	1	7.42E-14
		M H H A P R L N P P V M	1	3.30E-15
		M H S H W Q R P Q S P F	1	2.91E-16
		M H H P V Y P F Q H P P	1	4.45E-16
		L T T H N T W F H H R S	1	6.65E-16
		L S H H K T V P I D A N	1	1.65E-15
		A H F G K P P H F G S S	1	3.66E-16
		M H R H L G P A L S D A	1	4.19E-16
		M H S P H R T L P I L T	1	5.95E-13
		Y H P R A L T P P T P L	1	8.27E-14

The probabilities of a peptide sequence's random occurrence in the parent library were calculated using INFO of the RELIC suite of programs (*30*) to determine if multiply occurring peptides were an inherent result of incomplete sequence representation or positional amino acid biases dictated by M13 phage biology of the parent Ph.D.-12 library (*39*). Each entry corresponds to a peptide from Table 1 without the C-terminal Cysteine. There is no correlation between how many times the peptide was recovered from the screen and the probability of occurrence in the parent Ph.D.-12 library.